INTROGRESSED GENOTYPES TO IMPROVE COMMON BEAN

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Introduction

Progress in common bean breeding requires the exploitation of genetic variation that is present among races or through introgression across gene pools. Iberian Peninsula is considered as a secondary center of genetic diversity (Santalla et al., 2002). Introgression from the Middle American to the Andean gene pool appears to be relatively common in Andean zones, while Middle American accessions from the Iberian Peninsula exhibit evidence of introgression from Andean beans (Chacón et al., 2005; Paredes and Gepts, 1995). This introgression was assumed to result from spontaneous outcrossing in farmers' fields, based on segregation found previously in farmers' varietal mixtures. Studies employing allozymes and DNA-based markers have revealed dozens of instances of natural introgression in plants, and morphological intermediary and molecular confirmation of introgression go hand by hand. The presence of crop-specific alleles in intermediate populations can help to provide strong evidence for a history of hybridization. The objective of the investigation presented here was to quantify the degree of spontaneous introgression on the phenotype of Mesoamerican landraces.

Material and Methods

One-hundred and sixty nine great northern cultivars were chosen for this study. The 23 parental cultivars, their 137 breeding lines and 9 controls were planted in four environments in the northwest of Spain during 2003-2004 seasons. Morphological, agronomical and seed quality traits were measured. Phaseolin seed protein, allozymes and microsatelites were studied. Principal component and canonical discriminant analysis were performed, and the classification criterion used was the allozyme cluster membership (Singh et al., 1991; Santalla et al., 2002).

Results and Discussion

Results from the multivariate analyses (Figure 1) consistently identified fifth internode length, number of nodes to first flower, leaflet length, seed yield and seed weight as major traits separating lines of Mesoamerican origin. The proportion of introgressed accessions in the Mesoamerican germplasm studied (33 out of 137, or 24%) was similar to the Middle American accessions with Andean phaseolin (33%) in the Middle American region but higher than the proportion of introgressed accessions (13%) in the Andean region. These great northern types (> 40 g/100 seeds) are common in the Iberian Peninsula and

are surrounded by landraces that are genetically Andean American. There is a higher probability that any outcrossing of these Mesoamerican types would involve Andean American germplasm. This might explain the surprisingly high frequency (24%) of introgressed Middle American types in this secondary center of diversity. Microsatellite approach seems to identify a molecular marker for these accessions. The introgressed genotypes are sufficiently productive to have survived in farmers' systems, possibly due to more effective disease resistance. These may represent unique genetic recombination events that could be of utility to breeders seeking to improve common bean.

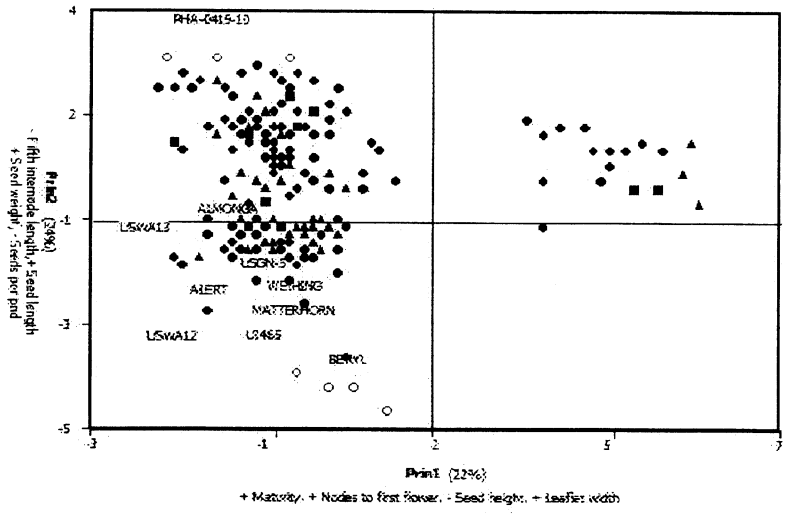

Fig. 1. Principal component analysis of diversity for Mesoamerican accessions.

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References

Chacón, M.I., S.B. Pickersgill & D.G. Debouck. 2005. Domestication patterns in common bean (*Phaseolus vulgaris* L.) and the origin of the Mesoamerican and Andean cultivated races. Theor Appl Genet 110: 432-444.

Santalla, M., A.P. Rodiño & A.M. De Ron, 2002. Allozyme evidence supporting southwestern Europe as a secondary center of genetic diversity for common bean. Theor Appl Genet 104: 934-944.

Singh S.P., P. Gepts & D. G. Debouck. 1991. Races of common bean (*Phaseolus vulgaris*, Fabaceae). Econ. Bot. 45(3): 379-396.